

10/526411

DT06 Rsc'd PC 0 0 2 MAR 2005

PF 53896

SEQUENCE LISTING

<110> SunGene GmbH & Co.KGaA
<120> Transgenic expression cassettes for expressing nucleic acids
in nonreproductive floral tissues of plants
<130> PF53896-AT
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<141>
<160> 36
<170> PatentIn Ver. 2.1
<210> 1
<211> 2039
<212> DNA
<213> *Arabidopsis thaliana*
<220>
<221> promoter
<222> (1)..(2039)
<223> 76L promoter (including 5'-untranslated region) of
gene locus At3g01980

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gtctctgatc ttattgcccattt cttgggtcgat gactttgaaa acgtccatga accaaccctcc 180
atcgaaagag atgttgcgtt tcttgcgtcac aagattcata tcagtggacca cttgtactac 240
ttccaataga gtccccatgtt ttttgcgttccatc atcaacccat tatttagcac cacaacaaa 300
caggaaactc ttgtttctca aaatctcttt gtttgcgttccatc atcaacccat tatttagcac cacaacaaa 360
agagacat ttatatttgcgtt ccacccatgaa acatacataaa ataaagatga atgttttgcgttccatc 420
aactctgtat ccacccatgaa acatacataaa ataaagatga atgttttgcgttccatc 480
tttacaaggg tatacgatggc ttttgcgttccatc atcaacccat tatttagcac cacaacaaa 540
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<210> 2
<211> 2180
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> promoter
<222> (1)..(2180)
<223> 84L promoter (including 5'-untranslated region) of
gene locus At1g63140

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aactcatata tatttcattc atggaaaagt ttaatcaata acaaatacta tcttcatttc 120
ataaaaagcct tggttcagat ttttccacac acatttaaaa gtgtttaag tttatcttat 180
acctttaagt acatttatga tttttttttt ctccttattaa ataagctgaa agattataga 240
taaatggttt tggttttatta aaaatgatgc attgaaaata taaaaggaca ttttatatat 300
agataactaca tgatttaggcc gatggAACCA aagatgagcg actcttcttg taacattgtg 360
tttgctacgc aatgctcggt ttttttttc tttagatcgag actttgcctg agattctgg 420
tttcttcgtat tggtgaatca tatatgtctt gccttctcat ataggttcaa cattgaccaa 480
caaaaactac ggggtgggat ttttttttgg ggtggagagt ggagactaac cttgaccctt 540
ttcatttgcata atgatttttc tttcttgcata gaactattgt ttgttatttgcgttca 600
tttggccgat gtgttttgcata atatgttttta aacaaggcact tactatcagc aatagcaaaa 660
gtaacatgat atttgcataat cccgttggaa attcatgtcc attattttgt atatataat 720
attatataat agtagaattt ggttatgtat tgcattttctt ctaaatctat gctttctaa 780
gttaaaaaaca ggcgcccata tgacgcacat aaatgtcgtat atttaagagg cactgcaagt 840
tgaacaaaaaa aaaaaaaagta taggcactgc aaaagttatc caacgtattt aagactaagg 900
actaaagatt caaagataat attcagaaaaa agaaaaaagaa aaaaagagaa gataatattc 960
ggaaacatcc acaagcattc taaatctaga aaacataaaat aatacagcaa agatgggat 1020
gaagatgatga tccaactcca tcacagattc tcaagacaga ttttagaaagt gtcaagctca 1080
ccaaaagggt tataggagac tgactgttta ttgaaatgtt ttctacacgt ggacgcactg 1140
atatcatatt aaaacctgat tggttgcata acattcacta actcataccca aacggtccaa 1200
acctatgtct ccattttctt aaatgttgcata ttgcatttcca tacctacttt gcatacatta 1260
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tatatcgatg taacacttta ggattgaatc aatatgaaaaa gttatacacc gaatttgcata 1380
gaaacgagta tagcttagac aaaatttgcata ttcttaat taagcggaaa aataattaaa 1440
cagagaccaa attaagcgat cttcttgcata tgaatcact aaagtaaaagt taacccgtta 1500
gttagatgtt aactattaa acaaagaaaaa ctccaaaccc aatttgagaaa ctactcaa 1560
atagaaacaa cacataatga ttcttagact accaatatca tattcaactt tggttcgatt 1620
cccttaaaaac aaaatataat taaccaataa aaataggcata taatcgattc agaaacaatt 1680
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atgaatccat caaagcataat aaattcaca cgtttaaaaa tggagtgttgcata 1860
accaacaatt tttagaccatt cacactgaat gagttatgact aacattcaca ttccacattca 1920
attagggaaat ttgtactaat gaacacacaa taaaagtgaa aacaaatctc tacatattct 1980
tgtacaccaa tcttatattatc atgatcattt taaatataca cgaatattaa ttttataat 2040
gaaaaatacg tgcccatatt ttaatttataa tatatattta gctatcaaattt attaggcata 2100
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<210> 3
<211> 1033
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> promoter
<222> (1)..(1033)
<223> 76S promoter (including 5'-untranslated region) of
gene locus At3g01980

<400> 3

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aagaaggcaa agtagagcaa gcaagcaagc aaagcatttt tcttatttta tattttgtt 120
cggattccac caccacttg aaaaattgac atgtcacaat gatttctat cctagtctt 180
tattattaa cactctcaca atcccattac tctacacac 240
gttttcaaaa atccactacc ctcccaccac ctagaatctt ttcttaccta ccaacaccc 300
cctttgttct ctttatata tggtccaact aaatcaataa gggaaagcat cttttgtt 360
ggaggaattg ctttcattct cactcttgc gtgtgatca atggactagc taataacaag 420
ttcctcctct atatattca aaagaatgga acagaaacat aaacgaaaga cagagtac 480
gatgttcatg attcattgtc tgcgtggagc tcccaaattgc tttttatgct tacatattca 540
taaccaacaa cggctattaa ttataaacc aaaaacacgaa ataagttgt agcaaagtga 600
aatttaggaat cttggagatg gatccattag tagtaggata ataggatatg atgaaattt 660
gttggggaaac agtgataact tacgcttgct tccggcgccg gggaaagttgg aaaacctaca 720
aagtacagaa atggatctgg gccttgaagt gggctttta ttaaagaaaa aaatacatct 780
ccggttatcaa tcaccatctt cttctatcta caaattaaag aaggtacaa cagaacgtgg 840
tggatcatgt gtttaggcat taattatttgc ttgttgc 900
cacagtccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga 960
atcaacttca ctccctccct cccttaagtc ttgtgaatc tgctgaattt tttataaag 1020
agttactttg gca 1033

<210> 4

<211> 1097

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> promoter

<222> (1)..(1097)

<223> 84S promoter (including 5'-untranslated region) of
gene locus At1g63140

<400> 4

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tcatattaaa acctgattgt ttgttgaaca ttcactaact cataccaaac ggtccaaacc 120
tatgtctcca ttttcttaaa tggatgtttc gattccatac ctactttgc tacattattt 180
aatgttttc ttaagtttg attaaaatta aatgagcaca atatcacagt cgaatggat 240
atcgatgtaa cacttttagga ttgaatcaat atgaaaaggat atacaccgaa ttgttgagaa 300
acgagtatag cttagacaaaa atttggttt cttaaattaa gcgaaaaat attaaacag 360
agaccaaatt aagcgttctt cttgaactga aatcaactaaa gtaaagttaa cccgttagt 420
gagtgttaac tatttaaaca aagaaaactc caaaccataat tgagaaacta ctcaaacata 480
gaaacaacac ataatgattc agtagctacc aatatcatat tcaactttgt ttcgattcct 540
ttaaaaacaaa atataattaa ccaaataaaaa taggtcataa tcgattcaga aacaatttca 600
tattctctc tagtttagtt cagtttcatc taccggagt tggatataat ctataattt 660
atcgcttattt accttaaaag cgtcctcaaa ccaacccaaa caaaaatagt tgcatcaatg 720
aatccatcaa agcatataaa ttccacaccgt cttaaaatgg agtggatgt gataagtacc 780
aacaattttt gaccattcac actgaatgag tatgactaac attcacattc acattcaatt 840
aggaaagttg tactaatgaa cacacaataa aagtggaaaac aaatctctac atattcttgc 900
acaccaatctt atatttagatg atcatattttt atatacacga atattaattt tataatgaa 960
aaatacggtc ccatattttt attaattttt atatttagt atcaaattt aggcatatg 1020
ttggtgaggt ttctgaggtt aaaaaatgac aaagtatgaa taccatctat accttttata 1080
cctatcttc tcgattt 1097

<210> 5

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
Oligonucleotide primer

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<400> 5
gaccctgtcc cacctccaa

19

<210> 6
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 6
tgagaactgc gattgttgc a

21

<210> 7
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 7
gtcgactatac ctctgcgcaa tgaat

25

<210> 8
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 8
cccgaaaat cgagaaagat aggtt

25

<210> 9
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 9
gtcgacaaag gttatagga gactg

25

<210> 10
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 10
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<210> 11
 <211> 1187
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (132)..(764)
 <223> coding for gene product of Arabidopsis thaliana
 gene locus At3g01980

<400> 11
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atctcactcc ctccctccct taagtcttgt tgaatctgct gaattgtttt ataaagagtt 120

actttggcaa a atg gaa aat ccg gcg aag aga gtg ttg atg aca tcc aac 170
 Met Glu Asn Pro Ala Lys Arg Val Leu Met Thr Ser Asn
 1 5 10

ggc gac gag gtg tcc cga aac atc gct ttc cat cta gcc aaa cac ggt 218
 Gly Asp Glu Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly
 15 20 25

tgc aag ttg gta atg atg gga aat gag ggt tcc cta agg agc att gta 266
 Cys Lys Leu Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val
 30 35 40 45

gac aag att aga gat tcc att gag gga gcc ttc cct gcc gat gtt ata 314
 Asp Lys Ile Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile
 50 55 60

gca ctc gac atg gaa tct gac tct gaa gtt gct ttt cat gcc gct gtc 362
 Ala Leu Asp Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val
 65 70 75

caa aag gca tgg gaa ctt tcc ggc cat ttc gat gct ttt ctc aac tct 410
 Gln Lys Ala Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser
 80 85 90

tat acc tac caa ggt tta att tgc ttc ttg ttt ttc act acc ctg cct 458
 Tyr Thr Tyr Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro
 95 100 105

ttg atg ctc ttg tgt gtt gat cat tcc ttt att caa caa tct ttc ttt 506
 Leu Met Leu Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe
 110 115 120 125

ctt gca gga aag gtg cag gac att ctt caa gtc tct caa gat gag ttc 554
 Leu Ala Gly Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe
 130 135 140

cac aga atc aca aag atc aat ctc acc gct cca tgg ttt ctc ttg aag 602
 His Arg Ile Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys
 145 150 155

gct gta gcc aca agg atg aag gac cat gga tca gga ggc tcc att gtc 650
 Ala Val Ala Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val
 160 165 170

ttc atg gcc act atc gcc agc gga gag agg gcg ctt tac cct ggc gct	698	
Phe Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala		
175 180 185		
gat gcc tac gct tca act tct gcc gct att cac cag ctc gtc cggt gta	746	
Asp Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val		
190 195 200 205		
tgc atc cta gct cct aat tagacacatc gcgttcgtaa cttgaatatg	794	
Cys Ile Leu Ala Pro Asn		
210		
tttggatg attgggttgc aggcattcgc catgagtctc gggaaagcaca agatacgggt	854	
caacatgatc tctagagggc tgcatttgc tgatgatcat acagttctg tggaaagaga	914	
ccgagcgcag aagctggtca aggacgctgc acccctcggc cagtggctca acccggacac	974	
agacctctac tccactgtta tctacttgc cagcgatggc tcacgcttca tgacaggcac	1034	
cactgtcttgc tggtatggag cgcaatccct tacgcgaccc cgtctcaaattt cttacatgtg	1094	
atcaatgcct agtattattta taattctatg ttgtgtgtaa aaagtgaata tgaatcaagt	1154	
ttgataact atggaggat gaataatcca tcc	1187	
<210> 12		
<211> 211		
<212> PRT		
<213> <i>Arabidopsis thaliana</i>		
<400> 12		
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1 5 10 15		
Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly Cys Lys Leu		
20 25 30		
Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val Asp Lys Ile		
35 40 45		
Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile Ala Leu Asp		
50 55 60		
Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val Gln Lys Ala		
65 70 75 80		
Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser Tyr Thr Tyr		
85 90 95		
Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro Leu Met Leu		
100 105 110		
Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe Leu Ala Gly		
115 120 125		
Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe His Arg Ile		
130 135 140		
Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys Ala Val Ala		
145 150 155 160		

Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val Phe Met Ala
 165 170 175
 Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp Ala Tyr
 180 185 190
 Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val Cys Ile Leu
 195 200 205
 Ala Pro Asn
 210

<210> 13
 <211> 1146
 <212> DNA
 <213> *Arabidopsis thaliana*
 <220>
 <221> CDS
 <222> (1)..(1143)
 <223> coding for transcript (cDNA) of gene locus
 At1g63140

<400> 13

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ctt	atc	aaa	gaa	gaa	caa	cgt	tat	cac	gaa	gat	acg	gtg	agc	ttg	caa	96
Leu	Ile	Lys	Glu	Glu	Gln	Arg	Tyr	His	Glu	Asp	Thr	Val	Ser	Leu	Gln	
	20						25						30			
gcg	gag	agg	att	ttg	cat	gcc	atg	acc	ttc	ccc	atg	gtt	ctc	aaa	act	144
Ala	Glu	Arg	Ile	Leu	His	Ala	Met	Thr	Phe	Pro	Met	Val	Leu	Lys	Thr	
	35						40				45					
gct	ttg	gag	ctt	ggc	gtt	atc	gac	atg	atc	act	tct	gta	gat	gac	ggc	192
Ala	Glu	Leu	Gly	Val	Ile	Asp	Met	Ile	Thr	Ser	Val	Asp	Asp	Gly		
	50						55			60						
gtg	tgg	ctc	tcg	cct	tct	gag	atc	gct	ctt	ggt	ctc	cca	acc	aag	ccc	240
Val	Trp	Leu	Ser	Pro	Ser	Glu	Ile	Ala	Leu	Gly	Leu	Pro	Thr	Lys	Pro	
	65						70			75			80			
acc	aat	ccg	gag	gca	cca	gta	ttg	ctg	gac	cg	atg	cta	gtt	ttg	tta	288
Thr	Asn	Pro	Glu	Ala	Pro	Val	Leu	Leu	Asp	Arg	Met	Leu	Val	Leu	Leu	
							85			90			95			
gcc	agc	cac	tca	atc	ttg	aag	tac	cgt	acg	gta	gaa	acc	gga	gat	aac	336
Ala	Ser	His	Ser	Ile	Leu	Lys	Tyr	Arg	Thr	Val	Glu	Thr	Gly	Asp	Asn	
							100			105			110			
att	gga	agt	aga	aag	acc	gag	agg	gtc	tat	gca	gct	gaa	ccg	gtt	tgc	384
Ile	Gly	Ser	Arg	Lys	Thr	Glu	Arg	Val	Tyr	Ala	Ala	Glu	Pro	Val	Cys	
	115						120				125					
acg	ttt	ttc	ttg	aac	cgc	gga	gat	ggc	ttg	ggc	tct	ctc	gcc	act	ttg	432
Thr	Phe	Phe	Leu	Asn	Arg	Gly	Asp	Gly	Leu	Gly	Ser	Leu	Ala	Thr	Leu	
	130						135				140					
ttc	atg	gta	ctc	caa	ggg	gaa	gtc	tgt	atg	aag	cct	tgg	gaa	cat	ctc	480
Phe	Met	Val	Leu	Gln	Gly	Glu	Val	Cys	Met	Lys	Pro	Trp	Glu	His	Leu	
	145						150			155			160			

aaa gac atg ata tta gaa gga aaa gat gca ttc acc tct gct cat ggc	528
Lys Asp Met Ile Leu Glu Gly Lys Asp Ala Phe Thr Ser Ala His Gly	
165 170 175	
atg agg ttt ttc gaa ctc att ggt tcg aac gaa caa ttc gct gaa atg	576
Met Arg Phe Phe Glu Leu Ile Gly Ser Asn Glu Gln Phe Ala Glu Met	
180 185 190	
ttt aac cgg gca atg tcg gaa gct tcc aca ttg att atg aag aag gtt	624
Phe Asn Arg Ala Met Ser Glu Ala Ser Thr Leu Ile Met Lys Lys Val	
195 200 205	
tta gaa gtt tac aaa gga ttc gaa gat gta aat act ttg gtg gat gtg	672
Leu Glu Val Tyr Lys Gly Phe Glu Asp Val Asn Thr Leu Val Asp Val	
210 215 220	
gga gga gga att gga aca atc ata ggt caa gtg act tcc aag tat cct	720
Gly Gly Gly Ile Gly Thr Ile Ile Gly Gln Val Thr Ser Lys Tyr Pro	
225 230 235 240	
cat att aaa ggc atc aat ttc gat cta gca tcg gtt tta gcc cat gct	768
His Ile Lys Gly Ile Asn Phe Asp Leu Ala Ser Val Leu Ala His Ala	
245 250 255	
cct ttt aat aaa gga gtg gag cat gtt tca gga gat atg ttt aaa gaa	816
Pro Phe Asn Lys Gly Val Glu His Val Ser Gly Asp Met Phe Lys Glu	
260 265 270	
att cca aaa gga gat gcc atc ttc atg aaa tgg ata cta cat gat tgg	864
Ile Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Leu His Asp Trp	
275 280 285	
act gac gaa gat tgt gta aag atc cta aaa aat tat tgg aaa agt ctt	912
Thr Asp Glu Asp Cys Val Lys Ile Leu Lys Asn Tyr Trp Lys Ser Leu	
290 295 300	
ccc gag aaa gga aaa gtg ata ata gtc gag gtg gtt acg ccc gag gaa	960
Pro Glu Lys Gly Lys Val Ile Ile Val Glu Val Val Thr Pro Glu Glu	
305 310 315 320	
cca aag att aac gac att tct tct aac att gtg ttc ggt atg gac atg	1008
Pro Lys Ile Asn Asp Ile Ser Ser Asn Ile Val Phe Gly Met Asp Met	
325 330 335	
ctg atg tta gca gta agc tca ggt ggt aag gag agg tct ctt tcc caa	1056
Leu Met Leu Ala Val Ser Ser Gly Gly Lys Glu Arg Ser Leu Ser Gln	
340 345 350	
ttc gag act cta gcc tct gat tcg ggt ttt ctt cgt tgt gaa atc att	1104
Phe Glu Thr Leu Ala Ser Asp Ser Gly Phe Leu Arg Cys Glu Ile Ile	
355 360 365	
tgt cat gcc ttc tca tat agt gtt atc gaa tta cac aaa tag	1146
Cys His Ala Phe Ser Tyr Ser Val Ile Glu Leu His Lys	
370 375 380	
<210> 14	
<211> 381	
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<213> <i>Arabidopsis thaliana</i>	
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Leu Ile Lys Glu Glu Gln Arg Tyr His Glu Asp Thr Val Ser Leu Gln	
20 25 30	

Ala Glu Arg Ile Leu His Ala Met Thr Phe Pro Met Val Leu Lys Thr
 35 40 45

Ala Leu Glu Leu Gly Val Ile Asp Met Ile Thr Ser Val Asp Asp Gly
 50 55 60

Val Trp Leu Ser Pro Ser Glu Ile Ala Leu Gly Leu Pro Thr Lys Pro
 65 70 75 80

Thr Asn Pro Glu Ala Pro Val Leu Leu Asp Arg Met Leu Val Leu Leu
 85 90 95

Ala Ser His Ser Ile Leu Lys Tyr Arg Thr Val Glu Thr Gly Asp Asn
 100 105 110

Ile Gly Ser Arg Lys Thr Glu Arg Val Tyr Ala Ala Glu Pro Val Cys
 115 120 125

Thr Phe Phe Leu Asn Arg Gly Asp Gly Leu Gly Ser Leu Ala Thr Leu
 130 135 140

Phe Met Val Leu Gln Gly Glu Val Cys Met Lys Pro Trp Glu His Leu
 145 150 155 160

Lys Asp Met Ile Leu Glu Gly Lys Asp Ala Phe Thr Ser Ala His Gly
 165 170 175

Met Arg Phe Phe Glu Leu Ile Gly Ser Asn Glu Gln Phe Ala Glu Met
 180 185 190

Phe Asn Arg Ala Met Ser Glu Ala Ser Thr Leu Ile Met Lys Lys Val
 195 200 205

Leu Glu Val Tyr Lys Gly Phe Glu Asp Val Asn Thr Leu Val Asp Val
 210 215 220

Gly Gly Gly Ile Gly Thr Ile Ile Gly Gln Val Thr Ser Lys Tyr Pro
 225 230 235 240

His Ile Lys Gly Ile Asn Phe Asp Leu Ala Ser Val Leu Ala His Ala
 245 250 255

Pro Phe Asn Lys Gly Val Glu His Val Ser Gly Asp Met Phe Lys Glu
 260 265 270

Ile Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Leu His Asp Trp
 275 280 285

Thr Asp Glu Asp Cys Val Lys Ile Leu Lys Asn Tyr Trp Lys Ser Leu
 290 295 300

Pro Glu Lys Gly Lys Val Ile Ile Val Glu Val Val Thr Pro Glu Glu
 305 310 315 320

Pro Lys Ile Asn Asp Ile Ser Ser Asn Ile Val Phe Gly Met Asp Met
 325 330 335

Leu Met Leu Ala Val Ser Ser Gly Gly Lys Glu Arg Ser Leu Ser Gln
 340 345 350

Phe Glu Thr Leu Ala Ser Asp Ser Gly Phe Leu Arg Cys Glu Ile Ile
 355 360 365

Cys His Ala Phe Ser Tyr Ser Val Ile Glu Leu His Lys
 370 375 380

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<210> 15
<211> 394
<212> DNA
<213> Brassica napus

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<222> (3)..(392)

<223> coding for Brassica homologue H2

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1 5 10 15

cac ggt tgt cgg ttg gtg ttg atg gga aac gag gct tct cta agg agc 95
His Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser
20 25 30

act gtg gac tac ata cga gtc tct gtt gat gga gcc ttc cca gtg gag 143
Thr Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu
35 40 45

ctc att gga gcc gac atg gaa qct qat agt gag gaa gat ttc tat gtt 191
Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val
50 55 60

gct gtc caa aag gca tgg act cgt cta gga tct ttg gat gct ttt gtc 239
Ala Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val
65 70 75

aac tgc tgt acc tac caa ggg aag atg cag gac att ctc cga gtg tct 287
Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser
80 85 90 95

gaa gat gag ttc aag aaa atc aca agg atc aat ctc acg gct aca tgg 335
Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp
100 105 110

ttt atc ttg aag gct gtg gca agc atg atg aag gag aat gga aca gga 383
Phe Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly
115 120 125

ggc tcc att gg 394
Gly Ser Ile
130

<210> 16

<211> 130

<212> PRT

<213> Brassica napus

<400> 16

Asn Gly Asp Glu Val Ser Arg Asn Ile Ala Ile Gln Leu Ala Lys His
1 5 10 15

Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser Thr
20 25 30

Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu Leu
35 40 45

Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val Ala
50 55 60

Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val Asn
65 70 75 80

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Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser Glu
85 90 95
Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp Phe
100 105 110
Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly Gly
115 120 125
Ser Ile
130

<210> 17
<211> 429
<212> DNA
<213> Brassica napus

<220>
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<222> (2)..(427)
<223> coding for Brassica homologue H3

<400> 17
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Glu Phe Ser Gly Arg Arg Phe Arg Thr Thr Leu Asn Leu Met Ala Asn
1 5 10 15
aag gtg ttg atg aca gac aac ggc gac cag gtt tcc cgg aac atc gct 97
Lys Val Leu Met Thr Asp Asn Gly Asp Gln Val Ser Arg Asn Ile Ala
20 25 30
atc caa cta gcc aaa cac ggt tgg cgg ttg gtg ttg atg gga aac gag 145
Ile Gln Leu Ala Lys His Gly Cys Arg Leu Val Leu Met Gly Asn Glu
35 40 45
gct tct cta agg agc act gtg gac tac ata cga ttc tct gat gat gga 193
Ala Ser Leu Arg Ser Thr Val Asp Tyr Ile Arg Phe Ser Asp Asp Gly
50 55 60
gcc ttc cca gtg gag ctc att gga gcc gac atg qaa gct gat agt gag 241
Ala Phe Pro Val Glu Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu
65 70 75 80
gaa gat ttc tat gtt gct gtc caa acg gca tgg act cgt cta gga tct 289
Glu Asp Phe Tyr Val Ala Val Gln Thr Ala Trp Thr Arg Leu Gly Ser
85 90 95
ttg gat gct ttt gtc aac tgc tgg acc tac caa ggg aag atg cag gac 337
Leu Asp Ala Phe Val Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp
100 105 110
att ctc cga gtg tct gaa gat gag ttc aag aaa atc aca cgg atc aat 385
Ile Leu Arg Val Ser Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn
115 120 125
ctc acg gct aca tgg ttt atc ttg aag gct gtg gca agc atg at 429
Leu Thr Ala Thr Trp Phe Ile Leu Lys Ala Val Ala Ser Met
130 135 140
<210> 18
<211> 142
<212> PRT
<213> Brassica napus

<400> 18

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				20				25				30			
Ile	Gln	Leu	Ala	Lys	His	Gly	Cys	Arg	Leu	Val	Leu	Met	Gly	Asn	Glu
				35			40					45			
Ala	Ser	Leu	Arg	Ser	Thr	Val	Asp	Tyr	Ile	Arg	Phe	Ser	Asp	Asp	Gly
				50			55			60					
Ala	Phe	Pro	Val	Glu	Leu	Ile	Gly	Ala	Asp	Met	Glu	Ala	Asp	Ser	Glu
				65		70			75			80			
Glu	Asp	Phe	Tyr	Val	Ala	Val	Gln	Thr	Ala	Trp	Thr	Arg	Leu	Gly	Ser
				85			90			95					
Leu	Asp	Ala	Phe	Val	Asn	Cys	Cys	Thr	Tyr	Gln	Gly	Lys	Met	Gln	Asp
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Ile	Leu	Arg	Val	Ser	Glu	Asp	Glu	Phe	Lys	Lys	Ile	Thr	Arg	Ile	Asn
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<213> Brassica napus

<220>

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<222> (3)..(419)

<223> coding for Brassica homologue H4

<400> 19

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Arg	Arg	Phe	Arg	Gly	Glu	Asn	Asn	Leu	Thr	Gly	Lys	Ile	Gln	Met			
1				5				10				15					
gta	tat	gca	gcc	gag	ccg	gtt	tgc	acg	ctt	ttc	tta	aaa	cat	ggt	cat	95	
Val	Tyr	Ala	Ala	Glu	Pro	Val	Cys	Thr	Leu	Phe	Leu	Lys	His	Gly	His		
				20			25					30					
gag	tcg	ggt	tca	ctc	atg	tcc	cta	ttc	atg	gtg	cac	cat	agc	caa	gtc	143	
Glu	Ser	Gly	Ser	Leu	Met	Ser	Leu	Phe	Met	Val	His	His	Ser	Gln	Val		
				35			40				45						
ttt	ttc	gaa	act	tgg	aca	cat	ttg	aaa	gat	ctg	ata	caa	gaa	gga	aaa	191	
Phe	Phe	Thr	Trp	Thr	His	Leu	Lys	Asp	Leu	Ile	Gln	Glu	Gly	Lys			
				50			55				60						
gat	aca	ttc	att	tct	gct	cat	ggc	atg	agg	atc	ttt	gaa	tac	atc	ggt	239	
Asp	Thr	Phe	Ile	Ser	Ala	His	Gly	Met	Arg	Ile	Phe	Glu	Tyr	Ile	Gly		
				65		70		75									
ttg	aat	gaa	caa	ttc	gct	tgt	atg	ttt	aac	cat	gca	atg	tca	gaa	tct	287	
Leu	Asn	Glu	Gln	Phe	Ala	Cys	Met	Phe	Asn	His	Ala	Met	Ser	Glu	Ser		
				80		85			90			95					
tct	acc	atg	atc	atg	aag	aag	att	tta	gaa	gtt	tac	aga	gga	ttc	gaa	335	
Ser	Thr	Met	Ile	Met	Lys	Lys	Ile	Leu	Glu	Val	Tyr	Arg	Gly	Phe	Glu		
				100			105				110						

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gat att aaa act ttg gtg gat att gga gga gga ctt ggc acc aca cta 383
Asp Ile Lys Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Thr Leu
115 120 125

aat ctg gtt act tcc aag tat cct cat ata agg gta taatttcgat 429
Asn Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val
130 135

taaaactc 436

<210> 20
<211> 139
<212> PRT
<213> Brassica napus

<400> 20
Arg Arg Phe Arg Gly Glu Asn Asn Leu Thr Gly Lys Ile Gln Met Val
1 5 10 15
Tyr Ala Ala Glu Pro Val Cys Thr Leu Phe Leu Lys His Gly His Glu
20 25 30
Ser Gly Ser Leu Met Ser Leu Phe Met Val His His Ser Gln Val Phe
35 40 45
Phe Glu Thr Trp Thr His Leu Lys Asp Leu Ile Gln Glu Gly Lys Asp
50 55 60
Thr Phe Ile Ser Ala His Gly Met Arg Ile Phe Glu Tyr Ile Gly Leu
65 70 75 80
Asn Glu Gln Phe Ala Cys Met Phe Asn His Ala Met Ser Glu Ser Ser
85 90 95
Thr Met Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp
100 105 110
Ile Lys Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Thr Leu Asn
115 120 125
Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val
130 135

<210> 21
<211> 418
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(417)
<223> coding for Brassica homologue H5

<400> 21
gct gaa ccg gtt tgc acg ctt ttt tta acc cgt ggt gac gac tcg ggt 48
Ala Glu Pro Val Cys Thr Leu Phe Leu Thr Arg Gly Asp Asp Ser Gly
1 5 10 15
act cac aag tcc ctc ttc atg ttg ctc aat agc caa gta ttt ttc aag 96
Thr His Lys Ser Leu Phe Met Leu Leu Asn Ser Gln Val Phe Phe Lys
20 25 30
aca tgg gat aat ctg aag ggt gtg ata caa gaa gga aaa gat gcg ttt
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe 144
35 40 45

agt tca gct cat ggc atg cca tta ttc gaa tac atc ggt ttg gat gag	192
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu	
50 55 60	
caa ttc gct ggt atg ttt aac cat gca atg gca gaa tct tct acc atc	240
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile	
65 70 75 80	
att atg aag aaa att tta gaa gtt tac aga gga ttc gaa gat gta aat	288
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn	
85 90 95	
act ttg gtg gat att gga gga gga ctt ggc acc gta cta aac ctt gtc	336
Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Val Leu Asn Leu Val	
100 105 110	
act tcc aag tat cct caa att aag ggt atc aat ttc gat tta acc atg	384
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met	
115 120 125	
gtt tta gcc aat gct cct tct tat cca gga gtg g	418
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val	
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20 25 30	
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe	
35 40 45	
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu	
50 55 60	
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile	
65 70 75 80	
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn	
85 90 95	
Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Val Leu Asn Leu Val	
100 105 110	
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met	
115 120 125	
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val	
130 135	

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<220>	
<223> Description of the artificial sequence: protein motif	

<220>
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<222> (4)
<223> E/Q-variation

<400> 23
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1 5 10

<210> 24
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: protein motif

<220>
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<222> (7)
<223> R/K-variation

<400> 24
Leu Ala Lys His Gly Cys Arg Leu Val
1 5

<210> 25
<211> 15
<212> PRT
<213> Artificial sequence

<220>
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<400> 25
Met Gly Asn Glu Xaa Ser Leu Arg Ser Xaa Val Asp Xaa Ile Arg
1 5 10 15

<210> 26
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: protein motif

<220>
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<222> (14)
<223> Q/E-variation

<400> 26
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Phe

<210> 27
<211> 17
<212> PRT
<213> Artificial sequence

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<220>
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<220>
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<222> (3)
<223> K/R-variation

<400> 27
Ile Thr Lys Ile Asn Leu Thr Ala Xaa Trp Phe Xaa Leu Lys Ala Val
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Ala

<210> 28
<211> 9
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<220>
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<400> 28
Ala Glu Pro Val Cys Thr Xaa Phe Leu
1 5

<210> 29
<211> 16
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1 5 10 15

<210> 30
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<212> PRT
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<220>
<223> Description of the artificial sequence: protein motif

<400> 30
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1 5 10

<210> 31
<211> 17
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<222> (8)
<223> V/I-variation

<220>
<221> VARIANT

<222> (13)
<223> K/R-variation

<400> 31

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1 5 10 15

Asp

<210> 32

<211> 11

<212> PRT

<213> Artificial sequence

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<223> Description of the artificial sequence: protein
motif

<220>

<221> VARIANT

<222> (5)

<223> V/I-variation

<400> 32

Thr Leu Val Asp Val Gly Gly Gly Xaa Gly Thr
1 5 10

<210> 33

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
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<400> 33

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21

<210> 34

<211> 21

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence:
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<400> 34

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21

<210> 35

<211> 19

<212> DNA

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<223> Description of the artificial sequence:
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<400> 35
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19

<210> 36
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<212> DNA
<213> Artificial sequence

<220>
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oligonucleotide primer

<400> 36
tgagaactgc gattgttgc a

21

SEQUENCE LISTING

<110> Klebsattel, Martin
Keetman, Ulrich
Herbers, Karin
Flachmann, Ralf
Sauer, Matt
Hillebrand, Heike

DT06 Rsc'd PCT/PTO 02 MAR 2005

<120> Transgenic expression cassettes for expressing nucleic acids in nonreproductive floral tissues of plants

<130> 13173-00009-US

<150> PCT/EP 2003/009594

<151> 2003-08-29

<150> DE 102 41 124.7

<151> 2002-09-03

<160> 36

<170> PatentIn version 3.3

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gtctctgatc ttatttgcatt ctgggtcgat gactttgaaa acgtccatga accaacctcc 180
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taaaagagta tggagagaaa gagaaaaacc tgggaggatt cattctcctg atgagcttgg 600
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ataacttacg	cttgcttccg	gcgcggggaa	agttggaaaa	cctacaaagt	acagaaatgg	1740
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catcttcttc	tatctacaaa	ttaaagaagg	taacaacaga	acgtgggtga	tcatgtgtt	1860
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gagctttgc	agccacttct	tatagttatt	tagaattgac	gatcaatca	atctcactcc	1980
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aagaaggcaa agtagagcaa gcaagcaagc aaagcatttt tcttatttta tattttgttg 120
cggattccac caccacttg aaaaatgac atgtcacaat gatttcgtat cctagtctt 180
tattttaa cactctcaca atcccattac tctacacctc tttcattaag tcaacacacg 240
gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccc 300
cctttgttct ctttatatat tggtccaact aaatcaataa gggaaagcat cttttgggtt 360
ggaggaattt ctttcattct cactcttgc gtgttgatca atggactago taataacaag 420
ttccctccct atatatttca aaagaatgga acagaaacat aaacgaaaga cagagtacct 480
gatgttgatg attcattgtc tgtctgggc tcccaaatgc cttttatgt tacatattca 540
taaccaacaa cggctattaa ttataaacca aaaacacgaa ataagttgt agcaaagtga 600
aatttaggaat cttggagatg gatccattag tagtaggata ataggatatg atgaaatttg 660
gttgggaac agtgataact tacgcttgct tccggcgccg ggaaagtgg aaaacctaca 720
aagtacagaa atggatctgg gccttgaagt ggctttta ttaaagaaaa aaatacatct 780
ccgttatcaa tcaccatctt cttctatcta caaattaaag aaggtaacaa cagaacgtgg 840
tggatcatgt ggtaggcat taatttatttgc ctttgcgttgc ccgtttgggt aacacacaga 900
cacagttccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga 960
atcaatctca ctccctccct cccttaagtc ttgttgaatc tgctgaattt ttttataaaag 1020
agttacttttqca 1033

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<210> 4
<211> 1097
<212> DNA
<213> Arabidopsis thaliana
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<220>
<221> promoter
<222> (1)..(1097)
<223> 84S promoter (including 5'-untranslated region) of
      gene locus At1g63140
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tcatattaaa acctgattgt ttgttgaaca ttcactaact cataccaaac ggtccaaacc 120
tatgtctcca ttttcttaaa tggtgatttc gattccatac ctactttgca tacattattg 180
aatgtgttgc ttaagttgtg attaaaatta aatgagcaca atatcacagt cgaatggtat 240
atcgatgtaa cactttagga ttgaatcaat atgaaaagtt atacaccgaa tttgtgagaa 300
acgagtatag cttagacaaa atttggaaaa cttaaattaa gcggaaaaat aattaaacag 360
agaccaaatt aagcgttctt ctgttaactga aatcactaaa gtaaagttaa cccgttagta 420
gagtgttaac tatttaaaca aagaaaaactc caaacccaa atgaaaacta ctcaaacata 480
gaaacaacac ataatgattc agtagctacc aatatcatat tcaactttgt ttcgattcct 540
ttaaaacaaa atataattaa ccaaataaaa taggtcataa tcgattcaga aacaatttca 600
tattcttctc tagtttagtt cagtttcatt ctaccggagt tgtatacaat ctataatttt 660
atcgcttatt accttaaaaag cgtcctcaaa ccaaccaaaa caaaaatagt tgcataatg 720
aatccatcaa agcatataaaa ttccacaccgt cttaaaatgg agtgggtatg gataagtacc 780
aacaatttta gaccattcac actgaatgag tatgactaac attcacattc acattcaatt 840
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aggaaaatgg tactaatgaa cacacaataa aagtggaaaac aaatctctac atattcttgt 900
acaccaatct atatttagatg atcattttaa atatacacga atattaattt tataaatgaa 960
aaatacgtgc ccatatttta attaattttat atatttagct atcaaataattt aggcatata 1020
ttggtgaggt ttctgagttt aaaaaatgac aaagtatgaa taccatctat acctttatta 1080
cctatcttcc tcgattt 1097

<210> 5
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 5
gaccctgtcc cacctccaa 19

<210> 6
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 6
tgagaactgc gattgttgc a 21

<210> 7
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 7
gtcgactatc ctctgcgcaa tgaat 25

<210> 8
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
Oligonucleotide primer

<400> 8
cccgggaaat cgagaaaat aggtt 25

<210> 9

<211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:
 Oligonucleotide primer

 <400> 9
 gtcgacaaaag ggttatagga gactg 25

 <210> 10
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:
 Oligonucleotide primer

 <400> 10
 gtcgaccatg tttcagagga tatgt 25

 <210> 11
 <211> 1187
 <212> DNA
 <213> *Arabidopsis thaliana*

 <220>
 <221> CDS
 <222> (132)..(764)
 <223> coding for gene product of *Arabidopsis thaliana*
 gene locus At3g01980

 <400> 11
 gttccggtaa gagctttgc agccactctt tatagttatt tagaattggc gatcaatca 60
 attcactcc ctccctccct taagtcttgt tgaatctgct gaattgtttt ataaagagtt 120
 acttggcaa a atg gaa aat ccg gcg aag aga gtg ttg atg aca tcc aac 170
 Met Glu Asn Pro Ala Lys Arg Val Leu Met Thr Ser Asn
 1 5 10
 ggc gac gag gtg tcc cga aac atc gct ttc cat cta gcc aaa cac ggt 218
 Gly Asp Glu Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly
 15 20 25
 tgc aag ttg gta atg atg gga aat gag ggt tcc cta agg agc att gta 266
 Cys Lys Leu Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val
 30 35 40 45
 gac aag att aga gat tcc att gag gga gcc ttc cct gcc gat gtt ata 314
 Asp Lys Ile Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile
 50 55 60
 gca ctc gac atg gaa tct gac tct gaa gtt gct ttt cat gcc gct gtc 362
 Ala Leu Asp Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val
 65 70 75
 caa aag gca tgg gaa ctt tcc ggc cat ttc gat gct ttt ctc aac tct 410
 Gln Lys Ala Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser
 80 85 90
 tat acc tac caa ggt tta att tgc ttc ttg ttt ttc act acc ctg cct 458
 Tyr Thr Tyr Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro
 95 100 105

ttt atg ctc ttg tgt gtt gat cat tcc ttt att caa caa tct ttc ttt	506
Leu Met Leu Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe	
110 115 120 125	
ctt gca gga aag gtg cag gac att ctt caa gtc tct caa gat gag ttc	554
Leu Ala Gly Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe	
130 135 140	
cac aga atc aca aag atc aat ctc acc gct cca tgg ttt ctc ttg aag	602
His Arg Ile Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys	
145 150 155	
gct gta gcc aca agg atg aag gac cat gga tca gga ggc tcc att gtc	650
Ala Val Ala Thr Arg Met Lys Asp His Gly Ser Gly Ser Ile Val	
160 165 170	
ttc atg gcc act atc gcc agc gga gag agg gcg ctt tac cct ggc gct	698
Phe Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala	
175 180 185	
gat gcc tac gct tca act tct gcc gct att cac cag ctc gtc cgg gta	746
Asp Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val	
190 195 200 205	
tgc atc cta gct cct aat tagacacatc gcgttcgtaa cttaatatgt	794
Cys Ile Leu Ala Pro Asn	
210	
tttggatg attgggttgc aggcattcaggc catgagtctc ggaaagcaca agatacgggt	854
caacatgatc tctagagggc tgcatttgc tgatgatgat acagttctg tggaaagaga	914
ccgagcgcag aagctggta aggacgctgc acccctggc cagtggctca acccggacac	974
agaccttac tccactgtta tctacttgc cagcgtggc tcacgttca tgacaggcac	1034
cactgtcttgc tggatggag cgcagtttgc tacgcgaccc cgtctaaat cctacatgt	1094
atcaatgcct agtattattaa taattctatg ttgtgttgc aaagtgtata tgaatcaatgt	1154
tttaataact atggaggat gaataatcca tcc	1187

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<210> 12
<211> 211
<212> PRT
<213> Arabidopsis thaliana
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<400> 12
Met Glu Asn Pro Ala Lys Arg Val Leu Met Thr Ser Asn Gly Asp Glu
      1           5           10           15
Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly Cys Lys Leu
      20          25          30
Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val Asp Lys Ile
      35          40          45
Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile Ala Leu Asp
      50          55          60
Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val Gln Lys Ala
      65          70          75          80
Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser Tyr Thr Tyr
      85          90          95
Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro Leu Met Leu
      100         105         110
Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe Leu Ala Gly
      115         120         125
Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe His Arg Ile
      130         135         140
Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys Ala Val Ala
      145         150         155         160
Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val Phe Met Ala
      165         170         175
Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp Ala Tyr
      180         185         190

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Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val Cys Ile Leu
 195 200 205
 Ala Pro Asn
 210

<210> 13
 <211> 1146
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> CDS
 <222> (1)..(1143)
 <223> coding for transcript (cDNA) of gene locus
 At1g63140

<400> 13
 atg gag aac cat ctt caa cat tcc tta acc atc att cct aaa ccg gat 48
 Met Glu Asn His Leu Gln His Ser Leu Thr Ile Ile Pro Lys Pro Asp
 1 5 10 15
 cta atc aaa gaa gaa caa cgt tat cac gaa gat acg gtg agc ttg caa 96
 Leu Ile Lys Glu Glu Gln Arg Tyr His Glu Asp Thr Val Ser Leu Gln
 20 25 30
 gcg gag agg att ttg cat gcc atg acc ttc ccc atg gtt ctc aaa act 144
 Ala Glu Arg Ile Leu His Ala Met Thr Phe Pro Met Val Leu Lys Thr
 35 40 45
 gct ttg gag ctt ggc gtt atc gac atg atc act tct gta gat gac ggc 192
 Ala Leu Glu Leu Gly Val Ile Asp Met Ile Thr Ser Val Asp Asp Gly
 50 55 60
 gtg tgg ctc tcg cct tct gag atc gct ctt ggt ctc cca acc aag ccc 240
 Val Trp Leu Ser Pro Ser Glu Ile Ala Leu Gly Leu Pro Thr Lys Pro
 65 70 75 80
 acc aat ccg gag gca cca gta ttg ctg gac cgg atg cta gtt ttg tta 288
 Thr Asn Pro Glu Ala Pro Val Leu Leu Asp Arg Met Leu Val Leu Leu
 85 90 95
 gcc agc cac tca atc ttg aag tac cgt acg gta gaa acc gga gat aac 336
 Ala Ser His Ser Ile Leu Lys Tyr Arg Thr Val Glu Thr Gly Asp Asn
 100 105 110
 att gga agt aga aag acc gag agg gtc tat gca gct gaa ccg gtt tgc 384
 Ile Gly Ser Arg Lys Thr Glu Arg Val Tyr Ala Ala Glu Pro Val Cys
 115 120 125
 acg ttt ttc ttg aac cgc gga gat ggc ttg ggc tct ctc gcc act ttg 432
 Thr Phe Phe Leu Asn Arg Gly Asp Gly Leu Gly Ser Leu Ala Thr Leu
 130 135 140
 ttc atg gta ctc caa ggg gaa gtc tgt atg aag cct tgg gaa cat ctc 480
 Phe Met Val Leu Gln Gly Glu Val Cys Met Lys Pro Trp Glu His Leu
 145 150 155 160
 aaa gac atg ata tta gaa gga aaa gat gca ttc acc tct gct cat ggc 528
 Lys Asp Met Ile Leu Glu Gly Lys Asp Ala Phe Thr Ser Ala His Gly
 165 170 175
 atg agg ttt ttc gaa ctc att ggt tcg aac gaa caa ttc gct gaa atg 576
 Met Arg Phe Phe Glu Leu Ile Gly Ser Asn Glu Gln Phe Ala Glu Met
 180 185 190
 ttt aac ccg gca atg tcg gaa gct tcc aca ttg att atg aag aag gtt 624
 Phe Asn Arg Ala Met Ser Glu Ala Ser Thr Leu Ile Met Lys Lys Val
 195 200 205
 tta gaa gtt tac aaa gga ttc gaa gat gta aat act ttg gtg gat gtg 672
 Leu Glu Val Tyr Lys Gly Phe Glu Asp Val Asn Thr Leu Val Asp Val
 210 215 220

gga gga gga att gga aca atc ata ggt caa gtg act tcc aag tat cct	720
Gly Gly Gly Ile Gly Thr Ile Ile Gly Gln Val Thr Ser Lys Tyr Pro	
225 230 235 240	
cat att aaa ggc atc aat ttc gat cta gca tcg gtt tta gcc cat gct	768
His Ile Lys Gly Ile Asn Phe Asp Leu Ala Ser Val Leu Ala His Ala	
245 250 255	
cct ttt aat aaa gga gtg gag cat gtt tca gga gat atg ttt aaa gaa	816
Pro Phe Asn Lys Gly Val Glu His Val Ser Gly Asp Met Phe Lys Glu	
260 265 270	
att cca aaa gga gat gcc atc ttc atg aaa tgg ata cta cat gat tgg	864
Ile Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Leu His Asp Trp	
275 280 285	
act gac gaa gat tgt gta aag atc cta aaa aat tat tgg aaa agt ctt	912
Thr Asp Glu Asp Cys Val Lys Ile Leu Lys Asn Tyr Trp Lys Ser Leu	
290 295 300	
ccc gag aaa gga aaa gtc ata ata gtc gag gtc gtt acg ccc gag gaa	960
Pro Glu Lys Gly Lys Val Ile Ile Val Glu Val Val Thr Pro Glu Glu	
305 310 315 320	
cca aag att aac gac att tct tct aac att gtc ttc ggt atg gac atg	1008.
Pro Lys Ile Asn Asp Ile Ser Ser Asn Ile Val Phe Gly Met Asp Met	
325 330 335	
ctg atg tta gca gta agc tca ggt ggt aag gag agg tct ctt tcc caa	1056
Leu Met Leu Ala Val Ser Ser Gly Gly Lys Glu Arg Ser Leu Ser Gln	
340 345 350	
ttc gag act cta gcc tct gat tcg ggt ttt ctt cgt tgt gaa atc att	1104
Phe Glu Thr Leu Ala Ser Asp Ser Gly Phe Leu Arg Cys Glu Ile Ile	
355 360 365	
tgt cat gcc ttc tca tat agt gtt atc gaa tta cac aaa tag	1146
Cys His Ala Phe Ser Tyr Ser Val Ile Glu Leu His Lys	
370 375 380	

<210> 14
 <211> 381
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 14	
Met Glu Asn His Leu Gln His Ser Leu Thr Ile Ile Pro Lys Pro Asp	
1 5 10 15	
Leu Ile Lys Glu Glu Gln Arg Tyr His Glu Asp Thr Val Ser Leu Gln	
20 25 30	
Ala Glu Arg Ile Leu His Ala Met Thr Phe Pro Met Val Leu Lys Thr	
35 40 45	
Ala Leu Glu Leu Gly Val Ile Asp Met Ile Thr Ser Val Asp Asp Gly	
50 55 60	
Val Trp Leu Ser Pro Ser Glu Ile Ala Leu Gly Leu Pro Thr Lys Pro	
65 70 75 80	
Thr Asn Pro Glu Ala Pro Val Leu Leu Asp Arg Met Leu Val Leu Leu	
85 90 95	
Ala Ser His Ser Ile Leu Lys Tyr Arg Thr Val Glu Thr Gly Asp Asn	
100 105 110	
Ile Gly Ser Arg Lys Thr Glu Arg Val Tyr Ala Ala Glu Pro Val Cys	
115 120 125	
Thr Phe Phe Leu Asn Arg Gly Asp Gly Leu Gly Ser Leu Ala Thr Leu	
130 135 140	
Phe Met Val Leu Gln Gly Glu Val Cys Met Lys Pro Trp Glu His Leu	
145 150 155 160	
Lys Asp Met Ile Leu Glu Gly Lys Asp Ala Phe Thr Ser Ala His Gly	
165 170 175	

Met Arg Phe Phe Glu Leu Ile Gly Ser Asn Glu Gln Phe Ala Glu Met
 180 185 190
 Phe Asn Arg Ala Met Ser Glu Ala Ser Thr Leu Ile Met Lys Lys Val
 195 200 205
 Leu Glu Val Tyr Lys Gly Phe Glu Asp Val Asn Thr Leu Val Asp Val
 210 215 220
 Gly Gly Gly Ile Gly Thr Ile Ile Gly Gln Val Thr Ser Lys Tyr Pro
 225 230 235 240
 His Ile Lys Gly Ile Asn Phe Asp Leu Ala Ser Val Leu Ala His Ala
 245 250 255
 Pro Phe Asn Lys Gly Val Glu His Val Ser Gly Asp Met Phe Lys Glu
 260 265 270
 Ile Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Leu His Asp Trp
 275 280 285
 Thr Asp Glu Asp Cys Val Lys Ile Leu Lys Asn Tyr Trp Lys Ser Leu
 290 295 300
 Pro Glu Lys Gly Lys Val Ile Ile Val Glu Val Val Thr Pro Glu Glu
 305 310 315 320
 Pro Lys Ile Asn Asp Ile Ser Ser Asn Ile Val Phe Gly Met Asp Met
 325 330 335
 Leu Met Leu Ala Val Ser Ser Gly Gly Lys Glu Arg Ser Leu Ser Gln
 340 345 350
 Phe Glu Thr Leu Ala Ser Asp Ser Gly Phe Leu Arg Cys Glu Ile Ile
 355 360 365
 Cys His Ala Phe Ser Tyr Ser Val Ile Glu Leu His Lys
 370 375 380

<210> 15
 <211> 394
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (3)..(392)
 <223> coding for Brassica homologue H2

<400> 15
 cc aac ggc gac gag gtt tcc cgg aac atc gct atc caa cta gcc aaa 47
 Asn Gly Asp Glu Val Ser Arg Asn Ile Ala Ile Gln Leu Ala Lys
 1 5 10 15
 cac ggt tgt cgg ttg gtg ttg atg gga aac gag gct tct cta agg agc 95
 His Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser
 20 25 30
 act gtg gac tac ata cga gtc tct gtt gat gga gcc ttc cca gtg gag 143
 Thr Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu
 35 40 45
 ctc att gga gcc gac atg gaa gct gat agt gag gaa gat ttc tat gtt 191
 Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val
 50 55 60
 gct gtc caa aag gca tgg act cgt cta gga tct ttg gat gct ttt gtc 239
 Ala Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val
 65 70 75
 aac tgc tgt acc tac caa ggg aag atg cag gac att ctc cga gtg tct 287
 Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser
 80 85 90 95
 gaa gat gag ttc aag aaa atc aca agg atc aat ctc acg gct aca tgg 335
 Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp
 100 105 110

ttt atc ttg aag gct gtg gca agc atg atg aag gag aat gga aca gga	383								
Phe Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly									
115	120	125		ggc tcc att gg	394	Gly Ser Ile		130	
125									
ggc tcc att gg	394								
Gly Ser Ile									
130									

<210> 16
 <211> 130
 <212> PRT
 <213> Brassica napus

<400> 16			
Asn Gly Asp Glu Val Ser Arg Asn Ile Ala Ile Gln Leu Ala Lys His			
1	5	10	15
Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser Thr			
20	25	30	
Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu Leu			
35	40	45	
Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val Ala			
50	55	60	
Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val Asn			
65	70	75	80
Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser Glu			
85	90	95	
Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp Phe			
100	105	110	
Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly Gly			
115	120	125	
Ser Ile			
130			

<210> 17
 <211> 429
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (2)..(427)
 <223> coding for Brassica homologue H3

<400> 17			
g gaa ttt tcg ggt cga cga ttt cgt act act ctg aat cta atg gcc aat	49		
Glu Phe Ser Gly Arg Arg Phe Arg Thr Thr Leu Asn Leu Met Ala Asn			
1	5	10	15
aag gtg ttg atg aca gac aac ggc gac cag gtt tcc cgg aac atc gct	97		
Lys Val Leu Met Thr Asp Asn Gly Asp Gln Val Ser Arg Asn Ile Ala			
20	25	30	
atc caa cta gcc aaa cac ggt tgt cgg ttg gtg atg gga aac gag	145		
Ile Gln Leu Ala Lys His Gly Cys Arg Leu Val Leu Met Gly Asn Glu			
35	40	45	
gct tct cta agg agc act gtg gac tac ata cga ttc tct gat gat gga	193		
Ala Ser Leu Arg Ser Thr Val Asp Tyr Ile Arg Phe Ser Asp Asp Gly			
50	55	60	
gcc ttc cca gtg gag ctc att gga gcc gac atg gaa gct gat agt gag	241		
Ala Phe Pro Val Glu Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu			
65	70	75	80

gaa gat ttc tat gtt gct gtc caa acg gca tgg act cgt cta gga tct	289
Glu Asp Phe Tyr Val Ala Val Gln Thr Ala Trp Thr Arg Leu Gly Ser	
85 90 95	
ttg gat gct ttt gtc aac tgc tgt acc tac caa ggg aag atg cag gac	337
Leu Asp Ala Phe Val Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp	
100 105 110	
att ctc cga gtg tct gaa gat gag ttc aag aaa atc aca cgg atc aat	385
Ile Leu Arg Val Ser Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn	
115 120 125	
ctc acg gct aca tgg ttt atc ttg aag gct gtg gca agc atg at	429
Leu Thr Ala Thr Trp Phe Ile Leu Lys Ala Val Ala Ser Met	
130 135 140	

<210> 18
<211> 142
<212> PRT
<213> Brassica napus

<400> 18	
Glu Phe Ser Gly Arg Arg Phe Arg Thr Thr Leu Asn Leu Met Ala Asn	
1 5 10 15	
Lys Val Leu Met Thr Asp Asn Gly Asp Gln Val Ser Arg Asn Ile Ala	
20 25 30	
Ile Gln Leu Ala Lys His Gly Cys Arg Leu Val Leu Met Gly Asn Glu	
35 40 45	
Ala Ser Leu Arg Ser Thr Val Asp Tyr Ile Arg Phe Ser Asp Asp Gly	
50 55 60	
Ala Phe Pro Val Glu Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu	
65 70 75 80	
Glu Asp Phe Tyr Val Ala Val Gln Thr Ala Trp Thr Arg Leu Gly Ser	
85 90 95	
Leu Asp Ala Phe Val Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp	
100 105 110	
Ile Leu Arg Val Ser Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn	
115 120 125	
Leu Thr Ala Thr Trp Phe Ile Leu Lys Ala Val Ala Ser Met	
130 135 140	

<210> 19
<211> 436
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (3)..(419)
<223> coding for Brassica homologue H4

<400> 19	
gt cga cga ttt cgt gga gaa aac aat cta act gga aag atc caa atg	47
Arg Arg Phe Arg Gly Glu Asn Asn Leu Thr Gly Lys Ile Gln Met	
1 5 10 15	
gta tat gca gcc gag ccg gtt tgc acg ctt ttc tta aaa cat ggt cat	95
Val Tyr Ala Ala Glu Pro Val Cys Thr Leu Phe Leu Lys His Gly His	
20 25 30	
gag tcg ggt tca ctc atg tcc cta ttc atg gtg cac cat agc caa gtc	143
Glu Ser Gly Ser Leu Met Ser Leu Phe Met Val His His Ser Gln Val	
35 40 45	

ttt ttc gaa act tgg aca cat ttg aaa gat ctg ata caa gaa gga aaa	191
Phe Phe Glu Thr Trp Thr His Leu Lys Asp Leu Ile Gln Glu Gly Lys	
50 55 60	
gat aca ttc att tct gct cat ggc atg agg atc ttt gaa tac atc ggt	239
Asp Thr Phe Ile Ser Ala His Gly Met Arg Ile Phe Glu Tyr Ile Gly	
65 70 75	
ttg aat gaa caa ttc gct tgt atg ttt aac cat gca atg tca gaa tct	287
Leu Asn Glu Gln Phe Ala Cys Met Phe Asn His Ala Met Ser Glu Ser	
80 85 90 95	
tct acc atg atc atg aag aag att tta gaa gtt tac aga gga ttc gaa	335
Ser Thr Met Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu	
100 105 110	
gat att aaa act ttg gtg gat att gga gga gga ctt ggc acc aca cta	383
Asp Ile Lys Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Thr Leu	
115 120 125	
aat ctg gtt act tcc aag tat cct cat ata agg gta taatttcgat	429
Asn Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val	
130 135	
taaactc	436

<210> 20
<211> 139
<212> PRT
<213> Brassica napus

<400> 20

Arg Arg Phe Arg Gly Glu Asn Asn Leu Thr Gly Lys Ile Gln Met Val	
1 5 10 15	
Tyr Ala Ala Glu Pro Val Cys Thr Leu Phe Leu Lys His Gly His Glu	
20 25 30	
Ser Gly Ser Leu Met Ser Leu Phe Met Val His His Ser Gln Val Phe	
35 40 45	
Phe Glu Thr Trp Thr His Leu Lys Asp Leu Ile Gln Glu Gly Lys Asp	
50 55 60	
Thr Phe Ile Ser Ala His Gly Met Arg Ile Phe Glu Tyr Ile Gly Leu	
65 70 75 80	
Asn Glu Gln Phe Ala Cys Met Phe Asn His Ala Met Ser Glu Ser Ser	
85 90 95	
Thr Met Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp	
100 105 110	
Ile Lys Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Thr Leu Asn	
115 120 125	
Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val	
130 135	

<210> 21
<211> 418
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)...(417)
<223> coding for Brassica homologue H5

<400> 21

gct gaa ccg gtt tgc acg ctt ttt tta acc cgt ggt gac gac tcg ggt	48
Ala Glu Pro Val Cys Thr Leu Phe Leu Thr Arg Gly Asp Asp Ser Gly	

1	5	10	15	
act cac aag tcc ctc ttc atg ttg ctc aat agc caa gta ttt ttc aag				96
Thr His Lys Ser Leu Phe Met Leu Leu Asn Ser Gln Val Phe Phe Lys				
20	25	30		
aca tgg gat aat ctg aag ggt gtg ata caa gaa gga aaa gat gcg ttt				144
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe				
35	40	45		
agt tca gct cat ggc atg cca tta ttc gaa tac atc ggt ttg gat gag				192
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu				
50	55	60		
caa ttc gct ggt atg ttt aac cat gca atg gca gaa tct tct acc atc				240
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile				
65	70	75	80	
att atg aag aaa att tta gaa gtt tac aga gga ttc gaa gat gta aat				288
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn				
85	90	95		
act ttg gtg gat att gga gga gga ctt ggc acc gta cta aac ctt gtc				336
Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Val Leu Asn Leu Val				
100	105	110		
act tcc aag tat cct caa att aag ggt atc aat ttc gat tta acc atg				384
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met				
115	120	125		
gtt tta gcc aat gct cct tct tat cca gga gtg g				418
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val				
130	135			

<210> 22
 <211> 139
 <212> PRT
 <213> Brassica napus

<400> 22				
Ala Glu Pro Val Cys Thr Leu Phe Leu Thr Arg Gly Asp Asp Ser Gly				
1	5	10	15	
Thr His Lys Ser Leu Phe Met Leu Leu Asn Ser Gln Val Phe Phe Lys				
20	25	30		
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe				
35	40	45		
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu				
50	55	60		
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile				
65	70	75	80	
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn				
85	90	95		
Thr Leu Val Asp Ile Gly Gly Leu Gly Thr Val Leu Asn Leu Val				
100	105	110		
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met				
115	120	125		
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val				
130	135			

<210> 23
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: protein

motif

<220>

<221> VARIANT

<222> (4)

<223> E/Q-variation

<400> 23

Asn Gly Asp Glu Val Ser Arg Asn Ile Ala
1 5 10

<210> 24

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> VARIANT

<222> (7)

<223> R/K-variation

<400> 24

Leu Ala Lys His Gly Cys Arg Leu Val
1 5

<210> 25

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> unsure

<222> (5)

<223> All occurrences of Xaa indicate any amino acid

<400> 25

Met Gly Asn Glu Xaa Ser Leu Arg Ser Xaa Val Asp Xaa Ile Arg
1 5 10 15

<210> 26

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> VARIANT

<222> (14)

<223> Q/E-variation

<400> 26

Thr Tyr Gln Gly Lys Xaa Gln Asp Ile Leu Xaa Val Ser Gln Asp Glu
1 5 10 15

Phe

<210> 27

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> VARIANT

<222> (3)

<223> K/R-variation

<400> 27

Ile Thr Lys Ile Asn Leu Thr Ala Xaa Trp Phe Xaa Leu Lys Ala Val
1 5 10 15

Ala

<210> 28

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> unsure

<222> (7)

<223> All occurrences of Xaa indicate any amino acid

<400> 28

Ala Glu Pro Val Cys Thr Xaa Phe Leu
1 5

<210> 29

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> unsure

<222> (5)

<223> All occurrences of Xaa indicate any amino acid

<400> 29

Glu Gly Lys Asp Xaa Phe Xaa Ser Ala His Gly Met Xaa Xaa Phe Glu
1 5 10 15

<210> 30

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif

<220>

<221> unsure

<222> (5)

<223> All occurrences of Xaa indicate any amino acid

<400> 30

Glu Gln Phe Ala Xaa Met Phe Asn Xaa Ala Met
1 5 10

<210> 31

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif

<220>

<221> VARIANT

<222> (8)

<223> V/I-variation

<220>

<221> VARIANT

<222> (13)

<223> K/R-variation

<400> 31

Ala Thr Xaa Ile Met Lys Lys Val Leu Glu Val Tyr Lys Gly Phe Glu
1 5 10 15

Asp

<210> 32

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif

<220>
<221> VARIANT
<222> (5)
<223> V/I-variation

<400> 32
Thr Leu Val Asp Val Gly Gly Gly Xaa Gly Thr
1 5 10

<210> 33
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 33
cacttttccc ggcaataaca t 21

<210> 34
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 34
atcaggaagt gatggagcat c 21

<210> 35
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 35
gaccctgtcc cacctccaa 19

<210> 36
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 36

tgagaactgc gattgttgc a